

# Structure and function of the N-terminal domain of the yeast telomerase reverse transcriptase

Hackenberg C., Hakanpää J., Klochkov V., Lebedev A., Chugunova A., Malyavko A., Zatsepin T., Mishin A., Zvereva M., Lamzin V., Dontsova O., Polshakov V.

Kazan Federal University, 420008, Kremlevskaya 18, Kazan, Russia

## Abstract

© The Author(s) 2017. The elongation of single-stranded DNA repeats at the 3'-ends of chromosomes by telomerase is a key process in maintaining genome integrity in eukaryotes. Abnormal activation of telomerase leads to uncontrolled cell division, whereas its down-regulation is attributed to ageing and several pathologies related to early cell death. Telomerase function is based on the dynamic interactions of its catalytic subunit (TERT) with nucleic acids-telomerase RNA, telomeric DNA and the DNA/RNA heteroduplex. Here, we present the crystallographic and NMR structures of the N-terminal (TEN) domain of TERT from the thermotolerant yeast *Hansenula polymorpha* and demonstrate the structural conservation of the core motif in evolutionarily divergent organisms. We identify the TEN residues that are involved in interactions with the telomerase RNA and in the recognition of the 'fork' at the distal end of the DNA product/RNA template heteroduplex. We propose that the TEN domain assists telomerase biological function and is involved in restricting the size of the heteroduplex during telomere repeat synthesis.

<http://dx.doi.org/10.1093/nar/gkx1275>

## References

- [1] Greider, C. W. and Blackburn, E. H. (1985) Identification of a specific telomere terminal transferase activity in tetrahymena extracts. *Cell*, 43, 405-413.
- [2] Schmidt, J. C. and Cech, T. R. (2015) Human telomerase: biogenesis, trafficking, recruitment, and activation. *Gene Dev.*, 29, 1095-1105.
- [3] Kim, N. W., Piatyszek, M. A., Prowse, K. R., Harley, C. B., West, M. D., Ho, P. L., Coviello, G. M., Wright, W. E., Weinrich, S. L. and Shay, J. W. (1994) Specific association of human telomerase activity with immortal cells and cancer. *Science*, 266, 2011-2015.
- [4] Shay, J. W. (2016) Role of telomeres and telomerase in aging and cancer. *Cancer Discov.*, 6, 584-593.
- [5] Armanios, M. and Blackburn, E. H. (2012) The telomere syndromes. *Nat. Rev. Genet.*, 13, 693-704.
- [6] Armstrong, C. A. and Tomita, K. (2017) Fundamental mechanisms of telomerase action in yeasts and mammals: understanding telomeres and telomerase in cancer cells. *Open Biol.*, 7, 160338.
- [7] Miracco, E. J., Jiang, J., Cash, D. D. and Feigon, J. (2014) Progress in structural studies of telomerase. *Curr. Opin. Struct. Biol.*, 24, 115-124.
- [8] Jiang, J., Miracco, E. J., Hong, K., Eckert, B., Chan, H., Cash, D. D., Min, B., Zhou, Z. H., Collins, K. and Feigon, J. (2013) The architecture of Tetrahymena telomerase holoenzyme. *Nature*, 496, 187-192.
- [9] Wyatt, H. D. M., West, S. C. and Beattie, T. L. (2010) InTERTpreting telomerase structure and function. *Nucleic Acids Res.*, 38, 5609-5622.

- [10] Gillis, A. J., Schuller, A. P. and Skordalakes, E. (2008) Structure of the *Tribolium castaneum* telomerase catalytic subunit TERT. *Nature*, 455, 633-637.
- [11] Harkisheimer, M., Mason, M., Shuvaeva, E. and Skordalakes, E. (2013) A motif in the vertebrate telomerase N-terminal linker of TERT contributes to RNA binding and telomerase activity and processivity. *Structure*, 21, 1870-1878.
- [12] Jacobs, S. A., Podell, E. R. and Cech, T. R. (2006) Crystal structure of the essential N-terminal domain of telomerase reverse transcriptase. *Nat. Struct. Mol. Biol.*, 13, 218-225.
- [13] Mitchell, M., Gillis, A., Futahashi, M., Fujiwara, H. and Skordalakes, E. (2010) Structural basis for telomerase catalytic subunit TERT binding to RNA template and telomeric DNA. *Nat. Struct. Mol. Biol.*, 17, 513-518.
- [14] Rouda, S. and Skordalakes, E. (2007) Structure of the RNA-binding domain of telomerase: implications for RNA recognition and binding. *Structure*, 15, 1403-1412.
- [15] Huang, J., Brown, A. F., Wu, J., Xue, J., Bley, C. J., Rand, D. P., Wu, L., Zhang, R., Chen, J. J. L. and Lei, M. (2014) Structural basis for protein-RNA recognition in telomerase. *Nat. Struct. Mol. Biol.*, 21, 507-512.
- [16] Hoffman, H., Rice, C. and Skordalakes, E. (2017) Structural analysis reveals the deleterious effects of telomerase mutations in bone marrow failure syndromes. *J. Biol. Chem.*, 292, 4593-4601.
- [17] Chan, H., Wang, Y. and Feigon, J. (2017) Progress in human and *Tetrahymena* telomerase structure. *Annu. Rev. Biophys.*, 46, 199-225.
- [18] Sasaki, T. and Fujiwara, H. (2000) Detection and distribution patterns of telomerase activity in insects. *Eur. J. Biochem.*, 267, 3025-3031.
- [19] Fujiwara, H. (2014) In: Louis, EJ and Becker, MM (eds). *Subtelomeres*. Springer, Berlin, Heidelberg, Berlin, pp. 227-241.
- [20] Pardue, M.-L. and DeBaryshe, P. G. (2008) *Drosophila* telomeres: a variation on the telomerase theme. *Fly*, 2, 101-110.
- [21] Jacobs, S. A., Podell, E. R., Wuttke, D. S. and Cech, T. R. (2005) Soluble domains of telomerase reverse transcriptase identified by high-throughput screening. *Protein Sci.*, 14, 2051-2058.
- [22] Eckert, B. and Collins, K. (2012) Roles of Telomerase Reverse Transcriptase N-terminal Domain in Assembly and Activity of *Tetrahymena* Telomerase Holoenzyme. *J. Biol. Chem.*, 287, 12805-12814.
- [23] Akiyama, B. M., Parks, J. W. and Stone, M. D. (2015) The telomerase essential N-terminal domain promotes DNA synthesis by stabilizing short RNA-DNA hybrids. *Nucleic Acids Res.*, 43, 5537-5549.
- [24] Robart, A. R. and Collins, K. (2011) Human telomerase domain interactions capture DNA for TEN domain-dependent processive elongation. *Mol. Cell*, 42, 308-318.
- [25] Jurczyk, J., Nouwens, A. S., Holien, J. K., Adams, T. E., Lovrecz, G. O., Parker, M. W., Cohen, S. B. and Bryan, T. M. (2011) Direct involvement of the TEN domain at the active site of human telomerase. *Nucleic Acids Res.*, 39, 1774-1788.
- [26] Stern, J. L., Zyner, K. G., Pickett, H. A., Cohen, S. B. and Bryan, T. M. (2012) Telomerase recruitment requires both TCAB1 and Cajal bodies independently. *Mol. Cell. Biol.*, 32, 2384-2395.
- [27] Armbruster, B. N., Banik, S. S. R., Guo, C., Smith, A. C. and Counter, C. M. (2001) N-Terminal domains of the human telomerase catalytic subunit required for enzyme activity in vivo. *Mol. Cell. Biol.*, 21, 7775-7786.
- [28] Zaug, A. J., Podell, E. R., Nandakumar, J. and Cech, T. R. (2010) Functional interaction between telomere protein TPP1 and telomerase. *Gene Dev.*, 24, 613-622.
- [29] Wang, F., Podell, E. R., Zaug, A. J., Yang, Y. T., Baciu, P., Cech, T. R. and Lei, M. (2007) The POT1-TPP1 telomere complex is a telomerase processivity factor. *Nature*, 445, 506-510.
- [30] Latrick, C. M. and Cech, T. R. (2010) POT1-TPP1 enhances telomerase processivity by slowing primer dissociation and aiding translocation. *EMBO J.*, 29, 924-933.
- [31] Zhong, F. L., Batista, L. F. Z., Freund, A., Pech, M. F., Venteicher, A. S. and Artandi, S. E. (2012) TPP1 OB-fold domain controls telomere maintenance by recruiting telomerase to chromosome ends. *Cell*, 150, 481-494.
- [32] Malyavko, A. N., Parfenova, Y. Y., Zvereva, M. I. and Dontsova, O. A. (2014) Telomere length regulation in budding yeasts. *FEBS Lett.*, 588, 2530-2536.
- [33] Smekalova, E. M., Petrova, O. A., Zvereva, M. I. and Dontsova, O. A. (2012) *Hansenula Polymorpha* TERT: a telomerase catalytic subunit isolated in recombinant form with limited reverse transcriptase activity. *Acta naturae*, 4, 70-73.
- [34] Smekalova, E. M., Malyavko, A. N., Zvereva, M. I., Mardanov, A. V., Ravin, N. V., Skryabin, K. G., Westhof, E. and Dontsova, O. A. (2013) Specific features of telomerase RNA from *Hansenula polymorpha*. *RNA*, 19, 1563-1574.
- [35] Polshakov, V. I., Petrova, O. A., Parfenova, Y. Y., Efimov, S. V., Klochkov, V. V., Zvereva, M. I. and Dontsova, O. A. (2016) NMR assignments of the N-terminal domain of *Ogataea polymorpha* telomerase reverse transcriptase. *Biomol. NMR Assign.*, 10, 183-187.
- [36] Agaphonov, M., Romanova, N., Choi, E. S. and Ter-Avanesyan, M. (2010) A novel kanamycin/G418 resistance marker for direct selection of transformants in *Escherichia coli* and different yeast species. *Yeast*, 27, 189-195.

- [37] Bogdanova, A. I., Agaphonov, M. O. and Teravanesyan, M. D. (1995) Plasmid reorganization during integrative transformation in *Hansenula-Polymorpha*. *Yeast*, 11, 343-353.
- [38] Cianci, M., Bourenkov, G., Pompidor, G., Karpics, I., Kallio, J., Bento, I., Roessle, M., Cipriani, F., Fiedler, S. and Schneider, T. R. (2017) P13, the EMBL macromolecular crystallography beamline at the low-emittance PETRA III ring for high- and low-energy phasing with variable beam focusing. *J. Synchrotron. Radiat.*, 24, 323-332.
- [39] Kabsch, W. (2010) XDS. *Acta Crystallogr. D*, 66, 125-132.
- [40] Waterman, D. G., Winter, G., Parkhurst, J. M., Fuentes-Montero, L., Hattne, J., Brewster, A., Sauter, N. K., Evans, G. and Rosenstrom, P. (2013) The DIALS framework for integration software. *CCP4 Newslett. Protein Crystallogr.*, 49, 13-15.
- [41] Evans, P. R. and Murshudov, G. N. (2013) How good are my data and what is the resolution? *Acta Crystallogr. D*, 69, 1204-1214.
- [42] Winn, M. D., Ballard, C. C., Cowtan, K. D., Dodson, E. J., Emsley, P., Evans, P. R., Keegan, R. M., Krissinel, E. B., Leslie, A. G. W., McCoy, A. et al. (2011) Overview of the CCP4 suite and current developments. *Acta Crystallogr. D*, 67, 235-242.
- [43] Karplus, P. A. and Diederichs, K. (2012) Linking crystallographic model and data quality. *Science*, 336, 1030-1033.
- [44] Skubak, P. and Pannu, N. S. (2013) Automatic protein structure solution from weak X-ray data. *Nat. Commun.*, 4, 2777.
- [45] Sheldrick, G. M. (2010) Experimental phasing with SHELXC/D/E: combining chain tracing with density modification. *Acta Crystallogr. D*, 66, 479-485.
- [46] Guillot, B., Viry, L., Guillot, R., Lecomte, C. and Jelsch, C. (2001) Refinement of proteins at subatomic resolution with MOPRO. *J. Appl. Crystallogr.*, 34, 214-223.
- [47] Abrahams, J. P. and Leslie, A. G. W. (1996) Methods used in the structure determination of bovine mitochondrial F-1 ATPase. *Acta Crystallogr. D*, 52, 30-42.
- [48] Skubak, P., Waterreus, W.-J. and Pannu, N. S. (2010) Multivariate phase combination improves automated crystallographic model building. *Acta Crystallogr. D*, 66, 783-788.
- [49] Murshudov, G. N., Skubak, P., Lebedev, A. A., Pannu, N. S., Steiner, R. A., Nicholls, R. A., Winn, M. D., Long, F. and Vagin, A. A. (2011) REFMAC5 for the refinement of macromolecular crystal structures. *Acta Crystallogr. D*, 67, 355-367.
- [50] Cowtan, K. (2010) Recent developments in classical density modification. *Acta Crystallogr. D Biol. Crystallogr.*, 66, 470-478.
- [51] Cowtan, K. (2006) The Buccaneer software for automated model building. 1. Tracing protein chains. *Acta Crystallogr. D*, 62, 1002-1011.
- [52] Emsley, P., Lohkamp, B., Scott, W. G. and Cowtan, K. (2010) Features and development of Coot. *Acta Crystallogr. D*, 66, 486-501.
- [53] Lebedev, A. A. and Isupov, M. N. (2014) Space-group and origin ambiguity in macromolecular structures with pseudo-symmetry and its treatment with the program Zanuda. *Acta Crystallogr. D*, 70, 2430-2443.
- [54] Vagin, A. and Teplyakov, A. (1997) MOLREP: an automated program for molecular replacement. *J. Appl. Crystallogr.*, 30, 1022-1025.
- [55] Delaglio, F., Grzesiek, S., Vuister, G. W., Zhu, G., Pfeifer, J. and Bax, A. (1995) NMRPipe: a multidimensional spectral processing system based on UNIX pipes. *J. Biomol. NMR*, 6, 277-293.
- [56] Lee, W., Tonelli, M. and Markley, J. L. (2015) NMRFAM-SPARKY: enhanced software for biomolecular NMR spectroscopy. *Bioinformatics*, 31, 1325-1327.
- [57] Berjanskii, M. V. and Wishart, D. S. (2005) A Simple Method To Predict Protein Flexibility Using Secondary Chemical Shifts. *J. Am. Chem. Soc.*, 127, 14970-14971.
- [58] Shen, Y., Delaglio, F., Cornilescu, G. and Bax, A. (2009) TALOS plus: a hybrid method for predicting protein backbone torsion angles from NMR chemical shifts. *J. Biomol. NMR*, 44, 213-223.
- [59] Bardiaux, B., Malliavin, T. and Nilges, M. (2012) ARIA for solution and solid-state NMR. *Methods Mol. Biol.*, 831, 453-483.
- [60] Brunger, A. T., Adams, P. D., Clore, G. M., DeLano, W. L., Gros, P., Grosse-Kunstleve, R. W., Jiang, J. S., Kuszewski, J., Nilges, M., Pannu, N. S. et al. (1998) Crystallography & NMR system: A new software suite for macromolecular structure determination. *Acta Crystallogr. D Biol. Crystallogr.*, 54, 905-921.
- [61] Kuszewski, J., Gronenborn, A. M. and Clore, G. M. (1997) Improvements and extensions in the conformational database potential for the refinement of NMR and X-ray structures of proteins and nucleic acids. *J. Magn. Reson.*, 125, 171-177.
- [62] Laskowski, R. A., Rullmann, J. A., MacArthur, M. W., Kaptein, R. and Thornton, J. M. (1996) AQUA and PROCHECK-NMR: programs for checking the quality of protein structures solved by NMR. *J. Biomol. NMR*, 8, 477-486.

- [63] Lipari, G. and Szabo, A. (1982) Model-Free Approach To The Interpretation Of Nuclear Magnetic-Resonance Relaxation In Macromolecules.2. Analysis Of Experimental Results. *J. Am. Chem. Soc.*, 104, 4559-4570.
- [64] Farrow, N. A., Muhandiram, R., Singer, A. U., Pascal, S. M., Kay, C. M., Gish, G., Shoelson, S. E., Pawson, T., Forman-Kay, J. D. and Kay, L. E. (1994) Backbone dynamics of a free and phosphopeptide-complexed Src homology 2 domain studied by <sup>15</sup>N NMR relaxation. *Biochemistry*, 33, 5984-6003.
- [65] Clore, G. M., Szabo, A., Bax, A., Kay, L. E., Driscoll, P. C. and Gronenborn, A. M. (1990) Deviations from the simple 2-parameter model-free approach to the interpretation of <sup>15</sup>N nuclear magnetic relaxation of proteins. *J. Am. Chem. Soc.*, 112, 4989-4991.
- [66] Clore, G. M., Driscoll, P. C., Wingfield, P. T. and Gronenborn, A. M. (1990) Analysis of the backbone dynamics of interleukin-1 beta using two-dimensional inverse detected heteronuclear <sup>15</sup>N-<sup>1</sup>H NMR spectroscopy. *Biochemistry*, 29, 7387-7401.
- [67] Polshakov, V. I., Birdsall, B., Frenkiel, T. A., Gargaro, A. R. and Feeney, J. (1999) Structure and dynamics in solution of the complex of *Lactobacillus casei* dihydrofolate reductase with the new lipophilic antifolate drug trimetrexate. *Protein Sci.*, 8, 467-481.
- [68] Tillett, M. L., Blackledge, M. J., Derrick, J. P., Lian, L. Y. and Norwood, T. J. (2000) Overall rotational diffusion and internal mobility in domain II of protein G from *Streptococcus* determined from N-15 relaxation data. *Protein Sci.*, 9, 1210-1216.
- [69] Bosoy, D., Peng, Y., Mian, I. S. and Lue, N. F. (2003) Conserved N-terminal motifs of telomerase reverse transcriptase required for ribonucleoprotein assembly in vivo. *J. Biol. Chem.*, 278, 3882-3890.
- [70] Lai, C. K., Mitchell, J. R. and Collins, K. (2001) RNA Binding Domain of Telomerase Reverse Transcriptase. *Mol. Cell Biol.*, 21, 990-1000.
- [71] Krissinel, E. (2012) Enhanced fold recognition using efficient short fragment clustering. *J. Mol. Biochem.*, 1, 76-85.
- [72] Wallweber, G., Gryaznov, S., Pongracz, K. and Pruzan, R. (2003) Interaction of human telomerase with its primer substrate. *Biochemistry*, 42, 589-600.
- [73] Lue, N. F. (2005) A physical and functional constituent of telomerase anchor site. *J. Biol. Chem.*, 280, 26586-26591.
- [74] Romi, E., Baran, N., Gantman, M., Shmoish, M., Min, B., Collins, K. and Manor, H. (2007) High-resolution physical and functional mapping of the template adjacent DNA binding site in catalytically active telomerase. *Proc. Natl. Acad. Sci. U. S. A.*, 104, 8791-8796.
- [75] Bairley, R. C. B., Guillaume, G., Vega, L. R. and Friedman, K. L. (2011) A mutation in the catalytic subunit of yeast telomerase alters primer-template alignment while promoting processivity and protein-DNA binding. *J. Cell Sci.*, 124, 4241-4252.
- [76] O'Connor, C. M., Lai, C. K. and Collins, K. (2005) Two purified domains of telomerase reverse transcriptase reconstitute sequence-specific interactions with RNA. *J. Biol. Chem.*, 280, 17533-17539.
- [77] Wyatt, H. D. M., Lobb, D. A. and Beattie, T. L. (2007) Characterization of physical and functional anchor site interactions in human telomerase. *Mol. Cell Biol.*, 27, 3226-3240.
- [78] Xia, J. Q., Peng, Y., Mian, I. S. and Lue, N. F. (2000) Identification of functionally important domains in the N-terminal region of telomerase reverse transcriptase. *Mol. Cell Biol.*, 20, 5196-5207.
- [79] Wu, R. A. and Collins, K. (2014) Human telomerase specialization for repeat synthesis by unique handling of primer-template duplex. *EMBO J.*, 33, 921-935.
- [80] Wienken, C. J., Baaske, P., Rothbauer, U., Braun, D. and Duhr, S. (2010) Protein-binding assays in biological liquids using microscale thermophoresis. *Nat. Commun.*, 1, 100.
- [81] Sealey, D. C. F., Zheng, L., Taboski, M. A. S., Cruickshank, J., Ikura, M. and Harrington, L. A. (2010) The N-terminus of hTERT contains a DNA-binding domain and is required for telomerase activity and cellular immortalization. *Nucleic Acids Res.*, 38, 2019-2035.
- [82] Yen, W. F., Chico, L., Lei, M. and Lue, N. F. (2011) Telomerase regulatory subunit Est3 in two *Candida* species physically interacts with the TEN domain of TERT and telomeric DNA. *Proc. Natl. Acad. Sci. U. S. A.*, 108, 20370-20375.
- [83] Jiang, J., Chan, H., Cash, D. D., Miracco, E. J., Ogorzalek Loo, R. R., Upton, H. E., Cascio, D., O'Brien Johnson, R., Collins, K., Loo, J. A. et al. (2015) Structure of *Tetrahymena* telomerase reveals previously unknown subunits, functions, and interactions. *Science*, 350, aab4070.
- [84] Hong, K., Upton, H., Miracco, E. J., Jiang, J., Zhou, Z. H., Feigon, J. and Collins, K. (2013) *Tetrahymena* Telomerase Holoenzyme Assembly, Activation, and Inhibition by Domains of the p50 Central Hub. *Mol. Cell Biol.*, 33, 3962-3971.
- [85] Steczkiewicz, K., Zimmermann, M. T., Kurcinski, M., Lewis, B. A., Dobbs, D., Kloczkowski, A., Jernigan, R. L., Kolinski, A. and Ginalski, K. (2011) Human telomerase model shows the role of the TEN domain in advancing the double helix for the next polymerization step. *Proc. Natl. Acad. Sci. U. S. A.*, 108, 9443-9448.

- [86] Qi, X. D., Xie, M. Y., Brown, A. F., Bley, C. J., Podlevsky, J. D. and Chen, J. J. L. (2012) RNA/DNA hybrid binding affinity determines telomerase template-translocation efficiency. *EMBO J.*, 31, 150-161.
- [87] Forstemann, K. and Lingner, J. (2005) Telomerase limits the extent of base pairing between template RNA and telomeric DNA. *EMBO Rep.*, 6, 361-366.
- [88] Hammond, P. W. and Cech, T. R. (1998) Euplotes telomerase: Evidence for limited base-pairing during primer elongation and dGTP as an effector of translocation. *Biochemistry*, 37, 5162-5172.
- [89] Westover, K. D., Bushnell, D. A. and Kornberg, R. D. (2004) Structural basis of transcription: Separation of RNA from DNA by RNA polymerase II. *Science*, 303, 1014-1016.
- [90] Vassilyev, D. G., Vassilyeva, M. N., Perederina, A., Tahirov, T. H. and Artsimovitch, I. (2007) Structural basis for transcription elongation by bacterial RNA polymerase. *Nature*, 448, 157-162.
- [91] Kent, T., Kashkina, E., Anikin, M. and Temiakov, D. (2009) Maintenance of RNA-DNA Hybrid Length in Bacterial RNA Polymerases. *J. Biol. Chem.*, 284, 13497-13504.
- [92] Wu, R. A., Tam, J. and Collins, K. (2017) DNA-binding determinants and cellular thresholds for human telomerase repeat addition processivity. *EMBO J.*, 36, 1908-1927.